

## SEQUENCE LISTING

<110> Payne, Jewel  
Sick, August J.

<120> Novel *Bacillus thuringiensis* Isolate Active Against Lepidopteran  
Pests, and Genes Encoding Novel Lepidopteran-Active Toxins

<130> MA-43CDF2D4

<150> US 09/837,961  
<151> 2001-04-19

<150> US 09/521,344  
<151> 2000-03-09

<150> US 08/933,891  
<151> 1997-09-19

<150> US 08/356,034  
<151> 1994-12-14

<150> US 08/210,110  
<151> 1994-03-17

<150> US 07/865,168  
<151> 1992-04-09

<150> US 07/451,261  
<151> 1989-12-14

<150> US 371,955  
<151> 1989-06-27

<160> 10

<170> PatentIn version 3.2

<210> 1  
<211> 3528  
<212> DNA  
<213> *Bacillus thuringiensis*

<400> 1  
atgaataatc agaatcaatg cgttccttat aactgtttga atgatccgac aattgaaata 60  
ttagaaggag aaagaataga aactggttac accccaatag atatttcctt gtcgctaacg 120  
caatttctgt tgagtgaatt tgtcccaggt gctgggtttg tattaggttt aattgattta 180  
atatgggggt ttgtgggtcc ctctcaatgg gatgcatttc ttgtgcaaata tgaacagtta 240  
attaacaaaa gaatagagga attcgctagg aaccaagcaa tttctagatt agaagggcta 300  
agcaaccttt atcaaattta cgcagaagct tttagagagt gggaagcaga tcctactaat 360  
ccagcattaa cagaagagat gcgtattcag ttcaatgaca tgaacagtgc tcttacaacc 420

gctattcctc tttttacagt tcaaaattat caagtacctc ttctatcagt atatgttcaa	480
gctgcaaatt tacatttatac ggttttgaga gatgtttcag tgtttggaaca acgttgggga	540
tttgatgtag caacaatcaa tagtcgttat aatgatttaa ctaggcttat tggcacctat	600
acagattatg ctgtacgctg gtataatacg ggattagaac gtgtatgggg accggattct	660
agagattggg taagggtataa tcaattttaga agagagctaa cactaactgt attagatatac	720
gtttctctgt tcccgaacta tgatagtaga acgtatccaa ttcgaacagt ttcccaatta	780
actagagaaa ttatatacaa cccagtatta gaaaattttg atggtagttt tcgtggaatg	840
gctcagagaa tagaacagaa tattaggcaa ccacatctta tggatctcct taatagtata	900
accatttata ctgatgtgca tagaggcttt aattattggt caggacatca aataacagct	960
tctcctgtcg gttttgcggg gccagaattt acttttcccta gatatggaac catgggaaat	1020
gctgctccac ccgtactgat ctcaactact ggtttgggga tttttagaac attatcttca	1080
cctctttaca gaagaattat acttggttca ggcccaaata atcagaacct gtttgtcctt	1140
gatggaacgg aattttcttt tgctcccta acagccgatt taccttctac tatatacaga	1200
caaaggggaa cggtcgattc actagatgta ataccgccac aggataatag tgtgccagca	1260
cgtgcgggat ttagtcacg attaatgcat gttacaatgc tgagccaagc agctggagca	1320
gtttacacct tgagagctcc aacgttttct tggcgacatc gtagtgctga attctctaac	1380
ctaattcctt catcaciaat cacacagata cctttaacaa agtctattaa tcttggctct	1440
gggacctctg ttgttaaagg accaggattt acaggaggag atattcttcg aataacttca	1500
cctggccaga tttcaacctt aagagtgact attacggcac cattatcaca aagatatcgc	1560
gtaagaattc gctacgctt tactacaaat ttacaattcc atacatcaat tgacggaaga	1620
cctattaatc aggggaattt ttcagcaact atgagtagtg ggggtaattt acagtccgga	1680
agcttttagga ctgcagggtt tactactccg ttttaactttt caaatggatc aagtatattt	1740
acgttaagtg ctcatgtctt caattcaggc aatgaagttt atatagagcg aattgaattt	1800
gttccggcag aagtaacatt tgaggcgga tatgatttag aaagagcgca agaggcggg	1860
aatgctctgt ttacttcttc caatcaacta ggattaaaaa caaatgtgac ggactatcat	1920
attgatcaag tgtccaatct agtcgaatgt ttatccggtg aattctgtct ggatgaaaag	1980
agagaattgt ccgagaaagt caaacatgcg aaccgactca gtgatgagcg gaatttactt	2040
caagacccaa acttcagagg catcaataga caaccagacc gtggctggag aggcagtacg	2100

gatattacca	tccaaggagg	agatgacgta	ttcaaagaga	attacgtcac	actaccgggt	2160
acctttaatg	agtgttatcc	tacgtatctg	tatcaaaaaa	tagatgagtc	gaaattaaaa	2220
gcctataccc	gttaccaatt	aagagggtac	atcgaggata	gtcaacactt	agaaatctat	2280
ttaattcgct	acaatacaaa	acacgaaaca	gtaaatgtgc	caggtacggg	ttccttatgg	2340
ccgctttcag	tcgaaaatcc	aattggaaag	tgcggagaac	caaatcgatg	cgcaccacaa	2400
cttgaatgga	atcctgatct	agattgttcc	tgcagagacg	gggaaaaatg	tgcacatcac	2460
tcccatcatt	tctccttgga	cattgatatt	ggatgtacag	atttaaataga	gaacttaggt	2520
gtatgggtga	tattcaaaat	taagatgcaa	gatggtcacg	caagactagg	taatctagag	2580
tttctcgaag	agaaaccatt	agtaggcgaa	tcgttagcac	gcgtgaagag	agcggagaag	2640
aagtggagag	acaaacgaga	gaaattgcaa	gtggaaacaa	atatcgttta	taaagaggca	2700
aaagaatctg	tagatgcttt	atttgtgaac	tctcaatatg	atagattaca	agcggatacc	2760
gacatcgca	tgattcatgc	ggcagataaa	cgcgttcac	gaattcgaga	agcatatctt	2820
ccagagttat	ctgtaattcc	gggtgtcaat	gcgggcattt	ttgaagaatt	agagggacgt	2880
attttcacag	cctactcttt	atatgatgcg	agaaatgtca	ttaaaaatgg	cgatttcaat	2940
aatggcttat	catgctggaa	cgtgaaaggg	catgtagatg	tagaagaaca	aaacaaccac	3000
cgttcggttc	ttgttgtccc	ggaatgggaa	gcagaggtgt	cacaagaggt	tcgtgtctgt	3060
ccaggtcgtg	gctatatcct	acgtgttaca	gcgtacaaag	agggatatgg	agaaggttgc	3120
gtaacgattc	atgagatcga	agacaataca	gacgaactga	aattcagcaa	ctgtgtagaa	3180
gaggaagtat	atccaaacaa	cacggtaacg	tgtaatgatt	atactgcaaa	tcaagaagaa	3240
tacgggggtg	cgtacacttc	tcgtaatcgt	ggatatgggtg	aatcttatga	aagtaattct	3300
tccataccag	ctgagtatgc	gccagtttat	gaggaagcat	atatagatgg	aagaaaagag	3360
aatccttggtg	aatctaacag	aggatatggg	gattacacgc	cactaccagc	tggttatgtg	3420
acaaaagaat	tagagtactt	cccagaaacc	gataaggtat	ggattgagat	cggggaaacg	3480
gaaggaacat	tcatcgtgga	tagcgtggaa	ttactcctta	tggaggaa		3528

&lt;210&gt; 2

&lt;211&gt; 1176

&lt;212&gt; PRT

<213> *Bacillus thuringiensis*

&lt;400&gt; 2

Met Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Asn Asp Pro  
 1 5 10 15  
 Thr Ile Glu Ile Leu Glu Gly Glu Arg Ile Glu Thr Gly Tyr Thr Pro  
 20 25 30  
 Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser Glu Phe Val  
 35 40 45  
 Pro Gly Ala Gly Phe Val Leu Gly Leu Ile Asp Leu Ile Trp Gly Phe  
 50 55 60  
 Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu Gln Leu  
 65 70 75 80  
 Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser Arg  
 85 90 95  
 Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu Ala Phe Arg  
 100 105 110  
 Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Thr Glu Glu Met Arg  
 115 120 125  
 Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu  
 130 135 140  
 Phe Thr Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val Tyr Val Gln  
 145 150 155 160  
 Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser Val Phe Gly  
 165 170 175  
 Gln Arg Trp Gly Phe Asp Val Ala Thr Ile Asn Ser Arg Tyr Asn Asp  
 180 185 190  
 Leu Thr Arg Leu Ile Gly Thr Tyr Thr Asp Tyr Ala Val Arg Trp Tyr  
 195 200 205  
 Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg Asp Trp Val  
 210 215 220

Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val Leu Asp Ile  
 225 230 235 240

Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro Ile Arg Thr  
 245 250 255

Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val Leu Glu Asn  
 260 265 270

Phe Asp Gly Ser Phe Arg Gly Met Ala Gln Arg Ile Glu Gln Asn Ile  
 275 280 285

Arg Gln Pro His Leu Met Asp Leu Leu Asn Ser Ile Thr Ile Tyr Thr  
 290 295 300

Asp Val His Arg Gly Phe Asn Tyr Trp Ser Gly His Gln Ile Thr Ala  
 305 310 315 320

Ser Pro Val Gly Phe Ala Gly Pro Glu Phe Thr Phe Pro Arg Tyr Gly  
 325 330 335

Thr Met Gly Asn Ala Ala Pro Pro Val Leu Ile Ser Thr Thr Gly Leu  
 340 345 350

Gly Ile Phe Arg Thr Leu Ser Ser Pro Leu Tyr Arg Arg Ile Ile Leu  
 355 360 365

Gly Ser Gly Pro Asn Asn Gln Asn Leu Phe Val Leu Asp Gly Thr Glu  
 370 375 380

Phe Ser Phe Ala Ser Leu Thr Ala Asp Leu Pro Ser Thr Ile Tyr Arg  
 385 390 395 400

Gln Arg Gly Thr Val Asp Ser Leu Asp Val Ile Pro Pro Gln Asp Asn  
 405 410 415

Ser Val Pro Ala Arg Ala Gly Phe Ser His Arg Leu Ser His Val Thr  
 420 425 430

Met Leu Ser Gln Ala Ala Gly Ala Val Tyr Thr Leu Arg Ala Pro Thr  
 435 440 445

Phe Ser Trp Arg His Arg Ser Ala Glu Phe Ser Asn Leu Ile Pro Ser  
 450 455 460

Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Ile Asn Leu Gly Ser  
 465 470 475 480

Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu  
 485 490 495

Arg Ile Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg Val Thr Ile Thr  
 500 505 510

Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr  
 515 520 525

Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg Pro Ile Asn Gln  
 530 535 540

Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Gly Asn Leu Gln Ser Gly  
 545 550 555 560

Ser Phe Arg Thr Ala Gly Phe Thr Thr Pro Phe Asn Phe Ser Asn Gly  
 565 570 575

Ser Ser Ile Phe Thr Leu Ser Ala His Val Phe Asn Ser Gly Asn Glu  
 580 585 590

Val Tyr Ile Glu Arg Ile Glu Phe Val Pro Ala Glu Val Thr Phe Glu  
 595 600 605

Ala Glu Tyr Asp Leu Glu Arg Ala Gln Glu Ala Val Asn Ala Leu Phe  
 610 615 620

Thr Ser Ser Asn Gln Leu Gly Leu Lys Thr Asn Val Thr Asp Tyr His  
 625 630 635 640

Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser Gly Glu Phe Cys  
 645 650 655

Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Asn Arg  
 660 665 670

Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile  
 675 680 685

Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile  
 690 695 700

Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly  
 705 710 715 720

Thr Phe Asn Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu  
 725 730 735

Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu  
 740 745 750

Asp Ser Gln His Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Thr Lys His  
 755 760 765

Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Val  
 770 775 780

Glu Asn Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro Gln  
 785 790 795 800

Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys  
 805 810 815

Cys Ala His His Ser His His Phe Ser Leu Asp Ile Asp Ile Gly Cys  
 820 825 830

Thr Asp Leu Asn Glu Asn Leu Gly Val Trp Val Ile Phe Lys Ile Lys  
 835 840 845

Met Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu  
 850 855 860

Lys Pro Leu Val Gly Glu Ser Leu Ala Arg Val Lys Arg Ala Glu Lys  
 865 870 875 880

Lys Trp Arg Asp Lys Arg Glu Lys Leu Gln Val Glu Thr Asn Ile Val  
 885 890 895

Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln  
 900 905 910

Tyr Asp Arg Leu Gln Ala Asp Thr Asp Ile Ala Met Ile His Ala Ala  
 915 920 925

Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser  
 930 935 940

Val Ile Pro Gly Val Asn Ala Gly Ile Phe Glu Glu Leu Glu Gly Arg  
 945 950 955 960

Ile Phe Thr Ala Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn  
 965 970 975

Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val  
 980 985 990

Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu  
 995 1000 1005

Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg  
 1010 1015 1020

Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu  
 1025 1030 1035

Gly Cys Val Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu  
 1040 1045 1050

Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr  
 1055 1060 1065

Val Thr Cys Asn Asp Tyr Thr Ala Asn Gln Glu Glu Tyr Gly Gly  
 1070 1075 1080

Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Gly Glu Ser Tyr Glu Ser  
 1085 1090 1095

Asn Ser Ser Ile Pro Ala Glu Tyr Ala Pro Val Tyr Glu Glu Ala  
 1100 1105 1110



Tyr Ile Asp Gly Arg Lys Glu Asn Pro Cys Glu Ser Asn Arg Gly  
 1115 1120 1125

Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu  
 1130 1135 1140

Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly  
 1145 1150 1155

Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu  
 1160 1165 1170

Met Glu Glu  
 1175

<210> 3  
 <211> 3495  
 <212> DNA  
 <213> *Bacillus thuringiensis*

<400> 3  
 atggaaataa ataatcaaaa ccaatgtgtg ccttacaatt gtttaagtaa tcctaaggag 60  
 ataatattag gcgaggaaag gctagaaaca gggaatactg tagcagacat ttcattaggg 120  
 cttattaatt ttctatattc taattttgta ccaggaggag gatttatagt aggtttacta 180  
 gaattaatat ggggatttat agggccttcg caatgggata tttttttagc tcaaattgag 240  
 caattgatta gtcaaagaat agaagaattt gctaggaatc aggcaatttc aagattggag 300  
 gggctaagca atctttataa ggtctatggt agagcgttta gcgactggga gaaagatcct 360  
 actaatcctg ctttaaggga agaaatgcgt atacaattta atgacatgaa tagtgctctc 420  
 ataacggcta ttccactttt tagagttcaa aattatgaag ttgctctttt atctgtatat 480  
 gttcaagccg caaacttaca tttatctatt ttaagggatg tttcagtttt cggagaaaga 540  
 tggggatatg atacagcgac tatcaataat cgctatagtg atctgactag ccttattcat 600  
 gtttatacta accattgtgt ggatacgtat aatcagggat taaggcgttt ggaaggctgt 660  
 tttcttagcg attggattgt atataatcgt ttccggagac aattgacaat ttcagtatta 720  
 gatattgttg cgttttttcc aaattatgat attagaacat atccaattca aacagctact 780  
 cagctaacga ggggaagtcta tctggattta ccttttatta atgaaaatct ttctcctgca 840  
 gcaagctatc caaccttttc agctgctgaa agtgctataa ttagaagtcc tcatttagta 900  
 gactttttta atagctttac catttatata gatagtctgg cacgttatgc atattgggga 960

gggcacttgg	taaattcttt	ccgcacagga	accactacta	atttgataag	atcccccttta	1020
tatggaaggg	aaggaaatac	agagcgcccc	gtaactatta	ccgcatcacc	tagcgtacca	1080
atatttagaa	cactttcata	tattacaggc	cttgacaatt	caaatcctgt	agctggaatc	1140
gagggagtgg	aattccaaaa	tactataagt	agaagtatct	atcgtaaaag	cgggtccaata	1200
gattctttta	gtgaattacc	acctcaagat	gccagcgtat	ctcctgcaat	tgggtatagt	1260
caccgtttat	gccatgcaac	attttttagaa	cggattagt	gaccaagaat	agcaggcacc	1320
gtattttctt	ggacacaccg	tagtgccagc	cctactaatg	aagtaagtcc	atctagaatt	1380
acacaaattc	catgggtaaa	ggcgcatact	cttgcatctg	gtgcctccgt	cattaaaggt	1440
cctggattta	caggtggaga	tattctgact	aggaatagta	tgggcgagct	ggggacctta	1500
cgagtaacct	tcacaggaag	attaccacaa	agttattata	tacgtttccg	ttatgcttcg	1560
gtagcaaata	ggagtggtag	atthagatat	tcacagccac	cttcgtatgg	aatttcattt	1620
ccaaaaacta	tggacgcagg	tgaaccacta	acatctcggt	cgttcgctca	tacaacactc	1680
ttcactccaa	taaccttttc	acgagctcaa	gaagaatttg	atctatacat	ccaatcgggt	1740
gtttatatag	atcgaattga	atttataccg	gttactgcaa	catttgaggc	agaatatgat	1800
ttagaaagag	cgcaaaaggt	ggtgaatgcc	ctgtttacgt	ctacaaacca	actagggcta	1860
aaaacagatg	tgacggatta	tcataattgat	caggtatcca	atctagttgc	gtgtttatcg	1920
gatgaattht	gtctggatga	aaagagagaa	ttgtccgaga	aagttaaaca	tgcaaagcga	1980
ctcagtgatg	agcggaaattt	acttcaagat	ccaaacttca	gagggatcaa	taggcaacca	2040
gaccgtggct	ggagaggaag	tacggatatt	actatccaag	gaggagatga	cgtattcaaa	2100
gagaattacg	ttacgctacc	gggtaccttt	gatgagtgc	atccaacgta	tttatatcaa	2160
aaaatagatg	agtcgaaatt	aaaagcctat	accggttatc	aattaagagg	gtatatcgaa	2220
gatagtcaag	acttagaaat	ctatttaatt	cgttacaatg	caaaacacga	aatagtaa	2280
gtaccaggta	caggaagttt	atggcctctt	tctgtagaaa	atcaaattgg	accttgtgga	2340
gaaccgaatc	gatgcgcgcc	acaccttgaa	tggaatcctg	atttactctg	ttcctgcaga	2400
gacggggaaa	aatgtgcaca	tcattctcat	catttctctt	tggacattga	tgttggatgt	2460
acagacttaa	atgaggactt	aggtgtatgg	gtgatattca	agattaagac	gcaagatggc	2520
cacgcacgac	tagggaatct	agagtttctc	gaagagaaac	cattattagg	agaagcacta	2580
gctcgtgtga	aaagagcgga	gaaaaaatgg	agagacaaac	gcgaaacatt	acaattggaa	2640

```

acaactatcg tttataaaga ggcaaaagaa tctgtagatg ctttatttgt aaactctcaa 2700
tatgatagat tacaagcgga tacgaacatc gcgatgattc atgcggcaga taaacgcgtt 2760
catagaattc gagaagcgta tctgccggag ctgtctgtga ttccgggtgt caatgcggt 2820
atTTTTgaag aattagaaga gcgtattttc actgcatttt ccctatatga tgcgagaaat 2880
attattaaaa atggcgattt caataatggc ttattatgct ggaacgtgaa agggcatgta 2940
gaggtagaag aacaaaacaa tcaccgttca gtccctggta tcccagaatg ggaggcagaa 3000
gtgtcacaag aggttcgtgt ctgtccaggt cgtggctata tccttcgtgt tacagcgta 3060
aaagagggat atggagaagg ttgcgtaacg atccatgaga tcgagaacaa tacagacgaa 3120
ctgaaattca acaactgtgt agaagaggaa gtatatccaa acaacacggt aacgtgtatt 3180
aattatactg cgactcaaga agaatatgag ggtacgtaca cttctcgtaa tcgaggatat 3240
gacgaagcct atggtaataa cccttcgta ccagctgatt atgcgtcagt ctatgaagaa 3300
aatcgtata cagatagacg aagagagaat ccttgtgaat ctaacagagg atatggagat 3360
tacacaccac taccagctgg ttatgtaaca aaggaattag agtacttccc agagaccgat 3420
aaggatatga ttgagattgg agaaacagaa ggaacattca tcgtggacag cgtggaatta 3480
ctccttatgg aggaa 3495

```

<210> 4

<211> 1165

<212> PRT

<213> *Bacillus thuringiensis*

<400> 4

```

Met Glu Ile Asn Asn Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Ser
1           5           10           15

```

```

Asn Pro Lys Glu Ile Ile Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn
20           25           30

```

```

Thr Val Ala Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn
35           40           45

```

```

Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu Leu Ile Trp
50           55           60

```

```

Gly Phe Ile Gly Pro Ser Gln Trp Asp Ile Phe Leu Ala Gln Ile Glu
65           70           75           80

```

Gln Leu Ile Ser Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala Ile  
                     85                    90                    95

Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala  
                     100                    105                    110

Phe Ser Asp Trp Glu Lys Asp Pro Thr Asn Pro Ala Leu Arg Glu Glu  
                     115                    120                    125

Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Ile Thr Ala Ile  
                     130                    135                    140

Pro Leu Phe Arg Val Gln Asn Tyr Glu Val Ala Leu Leu Ser Val Tyr  
                     145                    150                    155                    160

Val Gln Ala Ala Asn Leu His Leu Ser Ile Leu Arg Asp Val Ser Val  
                     165                    170                    175

Phe Gly Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg Tyr  
                     180                    185                    190

Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn His Cys Val Asp  
                     195                    200                    205

Thr Tyr Asn Gln Gly Leu Arg Arg Leu Glu Gly Arg Phe Leu Ser Asp  
                     210                    215                    220

Trp Ile Val Tyr Asn Arg Phe Arg Arg Gln Leu Thr Ile Ser Val Leu  
                     225                    230                    235                    240

Asp Ile Val Ala Phe Phe Pro Asn Tyr Asp Ile Arg Thr Tyr Pro Ile  
                     245                    250                    255

Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp Leu Pro Phe  
                     260                    265                    270

Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser Tyr Pro Thr Phe Ser Ala  
                     275                    280                    285

Ala Glu Ser Ala Ile Ile Arg Ser Pro His Leu Val Asp Phe Leu Asn  
                     290                    295                    300

Ser Phe Thr Ile Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly  
 305 310 315 320

Gly His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn Leu Ile  
 325 330 335

Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr Glu Arg Pro Val Thr  
 340 345 350

Ile Thr Ala Ser Pro Ser Val Pro Ile Phe Arg Thr Leu Ser Tyr Ile  
 355 360 365

Thr Gly Leu Asp Asn Ser Asn Pro Val Ala Gly Ile Glu Gly Val Glu  
 370 375 380

Phe Gln Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro Ile  
 385 390 395 400

Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser Val Ser Pro Ala  
 405 410 415

Ile Gly Tyr Ser His Arg Leu Cys His Ala Thr Phe Leu Glu Arg Ile  
 420 425 430

Ser Gly Pro Arg Ile Ala Gly Thr Val Phe Ser Trp Thr His Arg Ser  
 435 440 445

Ala Ser Pro Thr Asn Glu Val Ser Pro Ser Arg Ile Thr Gln Ile Pro  
 450 455 460

Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val Ile Lys Gly  
 465 470 475 480

Pro Gly Phe Thr Gly Gly Asp Ile Leu Thr Arg Asn Ser Met Gly Glu  
 485 490 495

Leu Gly Thr Leu Arg Val Thr Phe Thr Gly Arg Leu Pro Gln Ser Tyr  
 500 505 510

Tyr Ile Arg Phe Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe  
 515 520 525

Arg Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys Thr Met  
 530 535 540

Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe Ala His Thr Thr Leu  
 545 550 555 560

Phe Thr Pro Ile Thr Phe Ser Arg Ala Gln Glu Glu Phe Asp Leu Tyr  
 565 570 575

Ile Gln Ser Gly Val Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr  
 580 585 590

Ala Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Val Val  
 595 600 605

Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr Asp Val  
 610 615 620

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Ala Cys Leu Ser  
 625 630 635 640

Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val Lys  
 645 650 655

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn  
 660 665 670

Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg Gly Ser Thr  
 675 680 685

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val  
 690 695 700

Thr Leu Pro Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln  
 705 710 715 720

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg  
 725 730 735

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr  
 740 745 750

Asn Ala Lys His Glu Ile Val Asn Val Pro Gly Thr Gly Ser Leu Trp  
 755 760 765

Pro Leu Ser Val Glu Asn Gln Ile Gly Pro Cys Gly Glu Pro Asn Arg  
 770 775 780

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg  
 785 790 795 800

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile  
 805 810 815

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile  
 820 825 830

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu  
 835 840 845

Phe Leu Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val Lys  
 850 855 860

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu  
 865 870 875 880

Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe  
 885 890 895

Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met  
 900 905 910

Ile His Ala Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu  
 915 920 925

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu  
 930 935 940

Leu Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn  
 945 950 955 960

Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Leu Cys Trp Asn Val  
 965 970 975

Lys Gly His Val Glu Val Glu Glu Gln Asn Asn His Arg Ser Val Leu  
                   980                                  985                                  990

Val Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys  
                   995                                  1000                                  1005

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly  
           1010                                  1015                                  1020

Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr  
           1025                                  1030                                  1035

Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu Glu Val Tyr Pro  
           1040                                  1045                                  1050

Asn Asn Thr Val Thr Cys Ile Asn Tyr Thr Ala Thr Gln Glu Glu  
           1055                                  1060                                  1065

Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Glu Ala  
           1070                                  1075                                  1080

Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr  
           1085                                  1090                                  1095

Glu Glu Lys Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu  
           1100                                  1105                                  1110

Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr  
           1115                                  1120                                  1125

Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp  
           1130                                  1135                                  1140

Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val  
           1145                                  1150                                  1155

Glu Leu Leu Leu Met Glu Glu  
           1160                                  1165

<210> 5  
 <211> 3567  
 <212> DNA  
 <213> Bacillus thuringiensis



<400> 5  
 atggaggaaa ataatcaaaa tcaatgcata ccttacaatt gtttaagtaa tcctgaagaa 60  
 gtacttttgg atggagaacg gatatcaact ggtaattcat caattgatat ttctctgtca 120  
 cttgttcagt ttctgggtatc taactttgta ccagggggag gatttttagt tggattaata 180  
 gattttgtat ggggaatagt tggcccttct caatgggatg catttctagt acaaattgaa 240  
 caattaatta atgaaagaat agctgaatth gctaggaatg ctgctattgc taatttagaa 300  
 ggattaggaa acaatttcaa tatatatgtg gaagcattta aagaatggga agaagatcct 360  
 aataatccag caaccaggac cagagtaatt gatcgctttc gtatacttga tgggctactt 420  
 gaaagggaca ttccttcgtt tcgaatttct ggatttgaag taccctttt atccgtttat 480  
 gctcaagcgg ccaatctgca tctagctata ttaagagatt ctgtaatttt tggagaaaga 540  
 tggggattga caacgataaa tgtcaatgaa aactataata gactaattag gcatattgat 600  
 gaatatgctg atcactgtgc aaatacgtat aatcggggat taaataattt accgaaatct 660  
 acgtatcaag attggataac atataatcga ttacggagag acttaacatt gactgtatta 720  
 gatatcgccg ctttctttcc aaactatgac aataggagat atccaattca gccagttggt 780  
 caactaaca ggggaagtta tacggacca ttaattaatt ttaatccaca gttacagtct 840  
 gtagctcaat tacctacttt taacgttatg gagagcagcg caattagaaa tcctcattta 900  
 tttgatatat tgaataatct tacaatcttt acggattggt ttagtggttg acgcaatttt 960  
 tattggggag gacatcgagt aatatctagc cttataggag gtggtaacat aacatctcct 1020  
 atatatggaa gagaggcgaa ccaggagcct ccaagatcct ttacttttaa tggaccggt 1080  
 tttaggactt tatcaaacc tactttacga ttattacagc aaccttggcc agcgccacca 1140  
 ttttaatttac gtggtgttga aggagtagaa ttttctacac ctacaaatag ctttacgtat 1200  
 cgaggaagag gtcaggttga ttctttaact gaattaccgc ctgaggataa tagtgtgcca 1260  
 cctcggaag gatatagtca tcgtttatgt catgcaactt ttgttcaaag atctggaaca 1320  
 ctttttttaa caactggtgt agtattttct tggacgcac gtagtgaac tcttacaat 1380  
 acaattgatc cagagagaat taatcaaata cttttagtga aaggatttag agtttggggg 1440  
 ggcacctctg tcattacagg accaggattt acaggagggg atatccttcg aagaaatacc 1500  
 tttggtgatt ttgtatctct acaagtcaat attaattcac caattacca aagataccgt 1560  
 ttaagatttc gttacgcttc cagtagggat gcacgagtta tagtattaac aggagcggca 1620  
 tccacaggag tgggaggcca agttagtgt aatatgcctc ttcagaaaac tatggaaata 1680

ggggagaact taacatctag aacatttaga tataccgatt ttagtaatcc tttttcattt	1740
agagctaate cagatataat tgggataagt gaacaacctc tatttggtgc aggttctatt	1800
agtagcgggtg aactttatat agataaaatt gaaattattc tagcagatgc aacatttgaa	1860
gcagaatctg atttagaaag agcacaaaag gcggtgaatg ccctgtttac ttcttccaat	1920
caaategggt taaaaaccga tgtgacggat tatcatattg atcaagtatc caatttagtg	1980
gattgtttat cagatgaatt ttgtctggat gaaaagcgag aattgtccga gaaagtcaaa	2040
catgcgaagc gactcagtga tgagcggaat ttacttcaag atccaaactt cagagggatc	2100
aatagacaac cagaccgtgg ctggagagga agtacagata ttaccatcca aggaggagat	2160
gacgtattca aagagaatta cgtcacacta ccgggtaccg ttgatgagtg ctatccaacg	2220
tatttatatc agaaaataga tgagtcgaaa ttaaaagctt ataccgtta tgaattaaga	2280
gggtatatcg aagatagtca agacttagaa atctatttga tccgttaca tgcaaaacac	2340
gaaatagtaa atgtgccagg cacgggttcc ttatggccgc tttcagccca aagtccaatc	2400
ggaaagtgtg gagaaccgaa tcgatgcgcg ccacaccttg aatggaatcc tgatctagat	2460
tgttcctgca gagacgggga aaaatgtgca catcattccc atcatttcac cttggatatt	2520
gatgttggat gtacagactt aaatgaggac ttaggtctat gggatgatt caagattaag	2580
acgcaagata accatgcaag actagggat ctagagtttc tcgaagagaa accattatta	2640
ggggaagcac tagctcgtgt gaaaagagcg gagaagaagt ggagagacaa acgagagaaa	2700
ctgcagttgg aaacaaatat tgtttataaa gaggcaaaag aatctgtaga tgctttattt	2760
gtaaactctc aatatgatag attacaagtg aatacgaaca tcgcaatgat tcatgcggca	2820
gataaacgcg ttcatagaat ccgggaagcg tatctgccag agttgtctgt gattccaggt	2880
gtcaatgcg ccatthtcga agaattagag ggacgtattt ttacagcgta ttccttatat	2940
gatgcgagaa atgtcattaa aaatggcgat ttcaataatg gcttattatg ctggaacgtg	3000
aaaggatcat tagatgtaga agagcaaaac aaccaccgtt cggtccttgt tatcccagaa	3060
tgggaggcag aagtgtcaca agaggttcgt gtctgtccag gtcgtggcta taccctcgt	3120
gtcacagcat ataaagaggg atatggagag ggctgcgtaa cgatccatga gatcgaagac	3180
aatacagacg aactgaaatt cagcaactgt gtagaagagg aagtatatcc aaacaacaca	3240
gtaacgtgta ataattatac tgggactcaa gaagaatatg agggtagcta cacttctcgt	3300
aatcaaggat atgacgaagc ctatggtaat aacccttcg taccagctga ttacgcttca	3360
gtctatgaag aaaaatcgta tacagatgga cgaagagaga atccttgtga atctaacaga	3420

ggctatggggg attacacacc actaccggct ggttatgtaa caaaggattt agagtacttc 3480  
 ccagagaccg ataaggtatg gattgagatc ggagaaacag aaggaacatt catcgtggat 3540  
 agcgtggaat tactccttat ggaggaa 3567

<210> 6  
 <211> 1189  
 <212> PRT  
 <213> *Bacillus thuringiensis*

<400> 6

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser  
 1 5 10 15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn  
 20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn  
 35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp  
 50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu  
 65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile  
 85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala  
 100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg  
 115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile  
 130 135 140

Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr  
 145 150 155 160

Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile  
 165 170 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr  
 180 185 190

Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn  
 195 200 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp  
 210 215 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu  
 225 230 235 240

Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile  
 245 250 255

Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile  
 260 265 270

Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn  
 275 280 285

Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu  
 290 295 300

Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe  
 305 310 315 320

Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn  
 325 330 335

Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg  
 340 345 350

Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr  
 355 360 365

Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg  
 370 375 380

Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr  
 385 390 395 400

Arg Gly Arg Gly Gln Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp  
 405 410 415

Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala  
 420 425 430

Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val  
 435 440 445

Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro  
 450 455 460

Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly  
 465 470 475 480

Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu  
 485 490 495

Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn  
 500 505 510

Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser  
 515 520 525

Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val  
 530 535 540

Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile  
 545 550 555 560

Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn  
 565 570 575

Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln  
 580 585 590

Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp  
 595 600 605

Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp  
 610 615 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn  
 625 630 635 640

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val  
 645 650 655

Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys  
 660 665 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu  
 675 680 685

Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro  
 690 695 700

Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp  
 705 710 715 720

Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu  
 725 730 735

Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys  
 740 745 750

Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp  
 755 760 765

Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn  
 770 775 780

Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile  
 785 790 795 800

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn  
 805 810 815

Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His  
 820 825 830

Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn  
 835 840 845

Glu Asp Leu Gly Leu Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Asn  
 850 855 860

His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu  
 865 870 875 880

Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp  
 885 890 895

Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala  
 900 905 910

Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu  
 915 920 925

Gln Val Asn Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val  
 930 935 940

His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly  
 945 950 955 960

Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala  
 965 970 975

Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn  
 980 985 990

Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu  
 995 1000 1005

Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala  
 1010 1015 1020

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile  
 1025 1030 1035

Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val  
 1040 1045 1050

Thr Ile His Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser  
 1055 1060 1065

Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys  
 1070 1075 1080

Asn Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr  
 1085 1090 1095

Ser Arg Asn Gln Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro Ser  
 1100 1105 1110

Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr  
 1115 1120 1125

Asp Gly Arg Arg Glu Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly  
 1130 1135 1140

Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu  
 1145 1150 1155

Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr  
 1160 1165 1170

Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu  
 1175 1180 1185

Glu

<210> 7  
 <211> 3522  
 <212> DNA  
 <213> *Bacillus thuringiensis*

<400> 7  
 atggagaata atattcaaaa tcaatgcgta ccttacaatt gtttaaataa tcctgaagta 60  
 gaaatattaa atgaagaaag aagtactggc agattaccgt tagatatatc cttatcgctt 120  
 acacgtttcc ttttgagtga atttgttcca ggtgtgggag ttgcgtttgg attatttgat 180  
 ttaatatggg gttttataac tccttctgat tggagcttat ttcttttaca gattgaacaa 240  
 ttgattgagc aaagaataga aacattggaa aggaaccggg caattactac attacgaggg 300  
 ttagcagata gctatgaaat ttatattgaa gcactaagag agtgggaagc aaatcctaata 360  
 aatgcacaat taagggaaga tgtgctgatt cgatttgcta atacagacga cgctttaata 420  
 acagcaataa ataattttac acttacaagt ttgaaatcc ctcttttatc ggtctatggt 480



caagcggcga atttacattt atcactatta agagacgctg tatcgtttgg gcagggttgg	540
ggactggata tagctactgt taataatcat tataatagat taataaatct tattcataga	600
tatacgaaac attgtttggg cacatacaat caaggattag aaaacttaag aggtactaat	660
actcgacaat gggcaagatt caatcagttt aggagagatt taacacttac tgtattagat	720
atcgttgctc tttttccgaa ctacgatggt agaacatata caattcaaac gtcacccaa	780
ttaacaaggg aaattttatac aagttcagta attgaggatt ctccagtttc tgctaataata	840
cctaattggtt ttaatagggc ggaatttggg gttagaccgc cccatcttat ggactttatg	900
aattctttgt ttgtaactgc agagactggt agaagtcaaa ctgtgtgggg aggacactta	960
gttagttcac gaaatacggc tggtaaccgt ataaatttcc ctagttacgg ggtcttcaat	1020
cctggtggcg ccatttggat tgcagatgag gatccacgtc ctttttatcg gacattatca	1080
gacctgtttt ttgtccgagg aggatttggg aatcctcatt atgtactggg gcttagggga	1140
gtagcatttc aacaaactgg tacgaaccac acccgaacat ttagaaatag tgggaccata	1200
gattctctag atgaaatccc acctcaggat aatagtgggg caccttgga tgattatagt	1260
catgtattaa atcatgttac atttgtacga tggccagggt agatttcagg aagtgattca	1320
tggagagctc caatgttttc ttggacgcac cgtagtgcaa cccctacaaa tacaattgat	1380
ccggagagga ttactcaaat accattggta aaagcacata cacttcagtc aggtactact	1440
gttgtaagag ggcccgggtt tacgggagga gatattcttc gacgaacaag tggaggacca	1500
tttgcttata ctattgttaa tataaatggg caattacccc aaaggatatcg tgcaagaata	1560
cgctatgcct ctactacaaa tctaagaatt tacgtaacgg ttgcagggtga acggattttt	1620
gctggtcaat ttaacaaaac aatggatacc ggtgacccat taacattcca atcttttagt	1680
tacgcaacta ttaatacagc ttttacattc ccaatgagcc agagtagttt cacagtaggt	1740
gctgatactt ttagttcagg gaatgaagtt tatatagaca gatttgaatt gattccagtt	1800
actgcaacat ttgaagcaga atatgattta gaaagagcac aaaaggcggg gaatgcgctg	1860
tttacttcta taaaccaa ataggataaaa acagatgtga cggattatca tattgatcaa	1920
gtatccaatt tagtggattg tttatcagat gaattttgtc tggatgaaaa gcgagaattg	1980
tccgagaaag tcaaacatgc gaagcgactc agtgatgagc ggaatttact tcaagatcca	2040
aacttcaaag gcatcaatag gcaactagac cgtgggttgg gaggaagtac ggatattacc	2100
atccaaagag gagatgacgt attcaaagaa aattatgtca cactaccagg tacctttgat	2160

```

gagtgcctatc caacgtatctt atatcaaaaa atagatgagt cgaaattaaa accctatact 2220
cgttatcaat taagagggta tatcgaggat agtcaagact tagaaatcta tttgatccgc 2280
tataatgcaa aacacgaaac agtaaagtgt ctaggtacgg gttctttatg gccgctttca 2340
gtccaaagtc caatcagaaa gtgtggagaa ccgaatcgat gcgcgccaca ccttgaatgg 2400
aatcctgata tagattgttc ctgcagagac ggggaaaaat gtgcacatca ttcgcatcat 2460
ttctccttgg acattgatgt tggatgtaca gacttaaattg aggacttaga tgtatgggtg 2520
atattcaaga ttaagacgca agatggccat gcaagactag gaaatctaga gtttctcgaa 2580
gagaaacat tagtcgggga agcactagct cgtgtgaaaa gagcagagaa aaaatggaga 2640
gataaacgtg aaaaattgga attggaaaca aatattgttt ataaaggaggc aaaagaatct 2700
gtagatgctt tatttgtaaa ctctcaatat gatcaattac aagcggatac gaatattgcc 2760
atgattcatg cggcagataa acgtgttcac agaattcggg aagcgtatct tccagagtta 2820
tctgtgattc cgggtgtaaa tgtagacatt ttcgaagaat taaaagggcg tattttcact 2880
gcattcttcc tatatgatgc gagaaatgtc attaaaaacg gtgatttcaa taatggctta 2940
tcatgctgga acgtgaaagg gcatgtagat gtagaagaac aaaacaacca ccgttcggtc 3000
cttggtgttc cggaatggga agcagaagtg tcacaagaag ttcgtgtctg tccgggtcgt 3060
ggctatatcc ttcgtgtcac agcgtacaag gagggatatg gagaagggtg cgtaaccatt 3120
catgagatcg agaacaatac agacgaactg aagtttagca actgcgtaga agaggaagtc 3180
tatccaaaca acacggtaac gtgtaatgat tatactgcaa atcaagaaga atacgggggt 3240
gcgtacactt cccgtaatcg tggatatgac gaaacttatg gaagcaattc ttctgtacca 3300
gctgattatg cgtcagtcta tgaagaaaaa tcgtatacag atggacgaag agacaatcct 3360
tgtgaatcta acagaggata tggggattac acaccactac cagctggcta tgtgacaaaa 3420
gaattagagt acttcccaga aaccgataag gtatggattg agatcggaga aacggaagga 3480
acattcatcg tggacagcgt ggaattactc cttatggagg aa 3522

```

<210> 8

<211> 1174

<212> PRT

<213> *Bacillus thuringiensis*

<400> 8

```

Met Glu Asn Asn Ile Gln Asn Gln Cys Val Pro Tyr Asn Cys Leu Asn
1           5           10           15

```

Asn Pro Glu Val Glu Ile Leu Asn Glu Glu Arg Ser Thr Gly Arg Leu  
 20 25 30

Pro Leu Asp Ile Ser Leu Ser Leu Thr Arg Phe Leu Leu Ser Glu Phe  
 35 40 45

Val Pro Gly Val Gly Val Ala Phe Gly Leu Phe Asp Leu Ile Trp Gly  
 50 55 60

Phe Ile Thr Pro Ser Asp Trp Ser Leu Phe Leu Leu Gln Ile Glu Gln  
 65 70 75 80

Leu Ile Glu Gln Arg Ile Glu Thr Leu Glu Arg Asn Arg Ala Ile Thr  
 85 90 95

Thr Leu Arg Gly Leu Ala Asp Ser Tyr Glu Ile Tyr Ile Glu Ala Leu  
 100 105 110

Arg Glu Trp Glu Ala Asn Pro Asn Asn Ala Gln Leu Arg Glu Asp Val  
 115 120 125

Arg Ile Arg Phe Ala Asn Thr Asp Asp Ala Leu Ile Thr Ala Ile Asn  
 130 135 140

Asn Phe Thr Leu Thr Ser Phe Glu Ile Pro Leu Leu Ser Val Tyr Val  
 145 150 155 160

Gln Ala Ala Asn Leu His Leu Ser Leu Leu Arg Asp Ala Val Ser Phe  
 165 170 175

Gly Gln Gly Trp Gly Leu Asp Ile Ala Thr Val Asn Asn His Tyr Asn  
 180 185 190

Arg Leu Ile Asn Leu Ile His Arg Tyr Thr Lys His Cys Leu Asp Thr  
 195 200 205

Tyr Asn Gln Gly Leu Glu Asn Leu Arg Gly Thr Asn Thr Arg Gln Trp  
 210 215 220

Ala Arg Phe Asn Gln Phe Arg Arg Asp Leu Thr Leu Thr Val Leu Asp  
 225 230 235 240

```

Ile Val Ala Leu Phe Pro Asn Tyr Asp Val Arg Thr Tyr Pro Ile Gln
      245                      250                      255

Thr Ser Ser Gln Leu Thr Arg Glu Ile Tyr Thr Ser Ser Val Ile Glu
      260                      265                      270

Asp Ser Pro Val Ser Ala Asn Ile Pro Asn Gly Phe Asn Arg Ala Glu
      275                      280                      285

Phe Gly Val Arg Pro Pro His Leu Met Asp Phe Met Asn Ser Leu Phe
      290                      295                      300

Val Thr Ala Glu Thr Val Arg Ser Gln Thr Val Trp Gly Gly His Leu
      305                      310                      315                      320

Val Ser Ser Arg Asn Thr Ala Gly Asn Arg Ile Asn Phe Pro Ser Tyr
      325                      330                      335

Gly Val Phe Asn Pro Gly Gly Ala Ile Trp Ile Ala Asp Glu Asp Pro
      340                      345                      350

Arg Pro Phe Tyr Arg Thr Leu Ser Asp Pro Val Phe Val Arg Gly Gly
      355                      360                      365

Phe Gly Asn Pro His Tyr Val Leu Gly Leu Arg Gly Val Ala Phe Gln
      370                      375                      380

Gln Thr Gly Thr Asn His Thr Arg Thr Phe Arg Asn Ser Gly Thr Ile
      385                      390                      395                      400

Asp Ser Leu Asp Glu Ile Pro Pro Gln Asp Asn Ser Gly Ala Pro Trp
      405                      410                      415

Asn Asp Tyr Ser His Val Leu Asn His Val Thr Phe Val Arg Trp Pro
      420                      425                      430

Gly Glu Ile Ser Gly Ser Asp Ser Trp Arg Ala Pro Met Phe Ser Trp
      435                      440                      445

Thr His Arg Ser Ala Thr Pro Thr Asn Thr Ile Asp Pro Glu Arg Ile
      450                      455                      460

```

Thr Gln Ile Pro Leu Val Lys Ala His Thr Leu Gln Ser Gly Thr Thr  
 465 470 475 480

Val Val Arg Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr  
 485 490 495

Ser Gly Gly Pro Phe Ala Tyr Thr Ile Val Asn Ile Asn Gly Gln Leu  
 500 505 510

Pro Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu  
 515 520 525

Arg Ile Tyr Val Thr Val Ala Gly Glu Arg Ile Phe Ala Gly Gln Phe  
 530 535 540

Asn Lys Thr Met Asp Thr Gly Asp Pro Leu Thr Phe Gln Ser Phe Ser  
 545 550 555 560

Tyr Ala Thr Ile Asn Thr Ala Phe Thr Phe Pro Met Ser Gln Ser Ser  
 565 570 575

Phe Thr Val Gly Ala Asp Thr Phe Ser Ser Gly Asn Glu Val Tyr Ile  
 580 585 590

Asp Arg Phe Glu Leu Ile Pro Val Thr Ala Thr Phe Glu Ala Glu Tyr  
 595 600 605

Asp Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ile  
 610 615 620

Asn Gln Ile Gly Ile Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln  
 625 630 635 640

Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu  
 645 650 655

Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp  
 660 665 670

Glu Arg Asn Leu Leu Gln Asp Pro Asn Phe Lys Gly Ile Asn Arg Gln  
 675 680 685

Leu Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Arg Gly  
 690 695 700

Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp  
 705 710 715 720

Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu  
 725 730 735

Lys Pro Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln  
 740 745 750

Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Val  
 755 760 765

Asn Val Leu Gly Thr Gly Ser Leu Trp Pro Leu Ser Val Gln Ser Pro  
 770 775 780

Ile Arg Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp  
 785 790 795 800

Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His  
 805 810 815

His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu  
 820 825 830

Asn Glu Asp Leu Asp Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp  
 835 840 845

Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu  
 850 855 860

Val Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg  
 865 870 875 880

Asp Lys Arg Glu Lys Leu Glu Leu Glu Thr Asn Ile Val Tyr Lys Glu  
 885 890 895

Ala Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Gln  
 900 905 910

Leu Gln Ala Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg  
 915 920 925

Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro  
 930 935 940

Gly Val Asn Val Asp Ile Phe Glu Glu Leu Lys Gly Arg Ile Phe Thr  
 945 950 955 960

Ala Phe Phe Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe  
 965 970 975

Asn Asn Gly Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu  
 980 985 990

Glu Gln Asn Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala  
 995 1000 1005

Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile  
 1010 1015 1020

Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val  
 1025 1030 1035

Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser  
 1040 1045 1050

Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys  
 1055 1060 1065

Asn Asp Tyr Thr Ala Asn Gln Glu Glu Tyr Gly Gly Ala Tyr Thr  
 1070 1075 1080

Ser Arg Asn Arg Gly Tyr Asp Glu Thr Tyr Gly Ser Asn Ser Ser  
 1085 1090 1095

Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys Ser Tyr Thr  
 1100 1105 1110

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly  
 1115 1120 1125

Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu  
 1130 1135 1140

Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr  
 1145 1150 1155

Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu  
 1160 1165 1170

Glu

<210> 9  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 42-mer oligonucleotide constructed to the sequence of the insert  
 in pM2,31-4

<400> 9  
 ggataccggt gaccattaa cattccaatc ttttagttac gc 42

<210> 10  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 40-mer oligonucleotide constructed to the sequence of the insert  
 in pM2,31-1

<400> 10  
 gaagtttatg gcctctttct gtagaaaatc aaattggacc 40